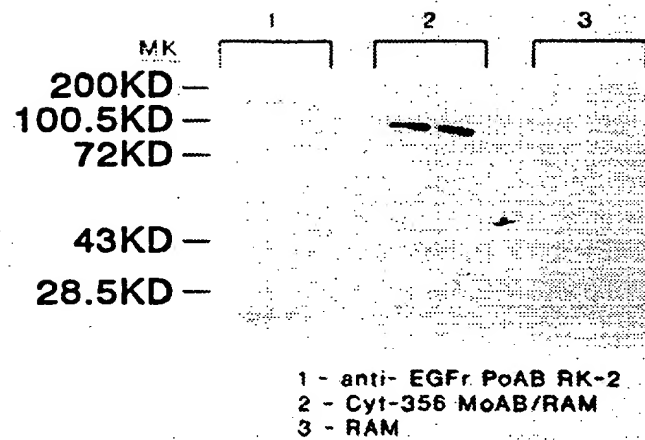


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FIGURE 1



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FIGURE 2A

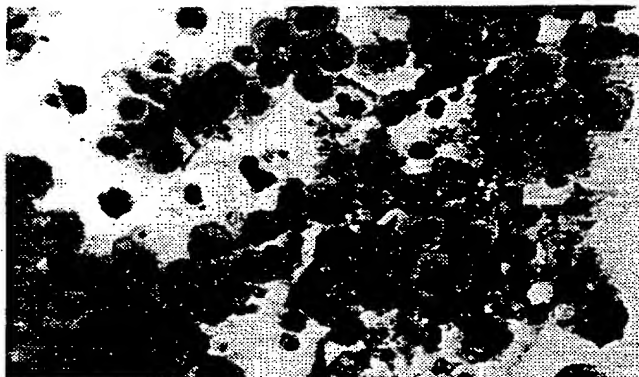


FIGURE 2B

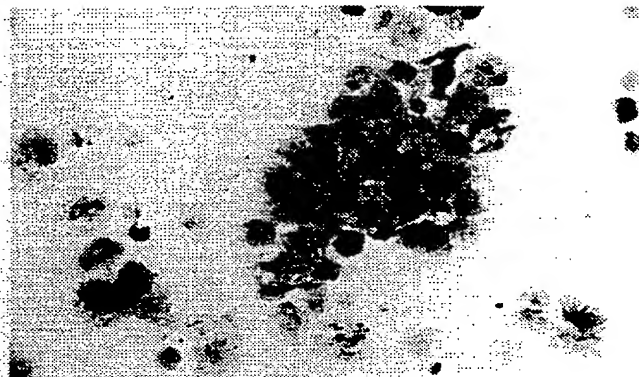


FIGURE 2C

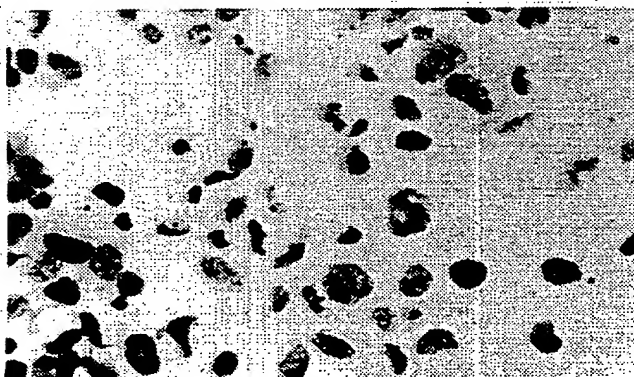
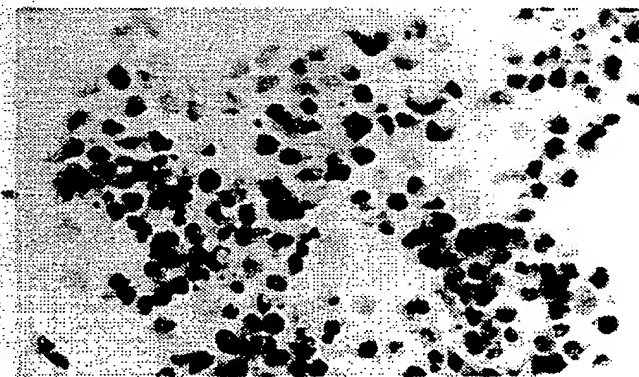


FIGURE 2D



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FIGURE 3A

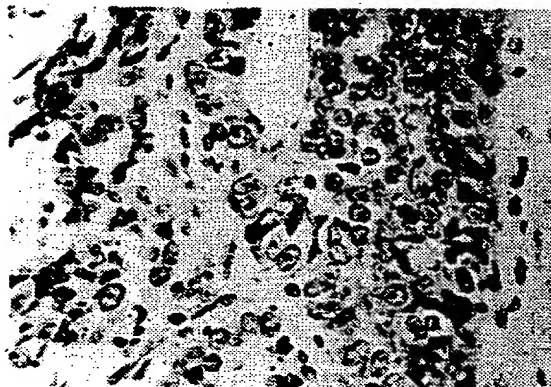


FIGURE 3B

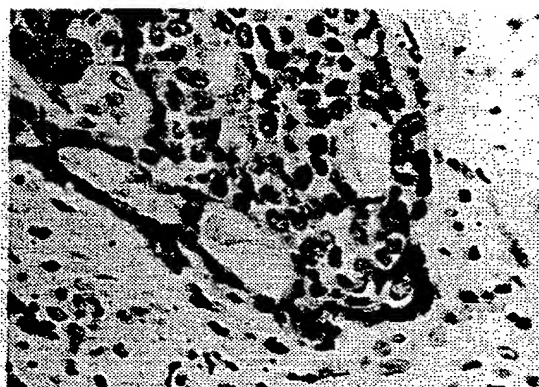


FIGURE 3C

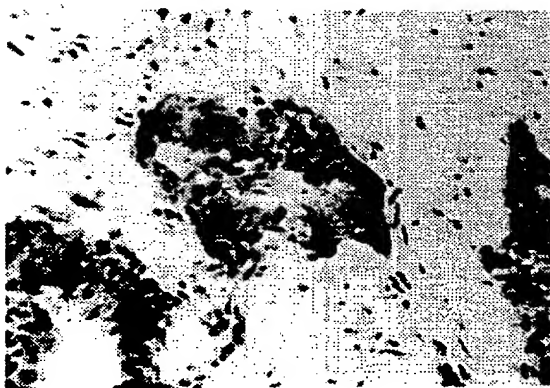
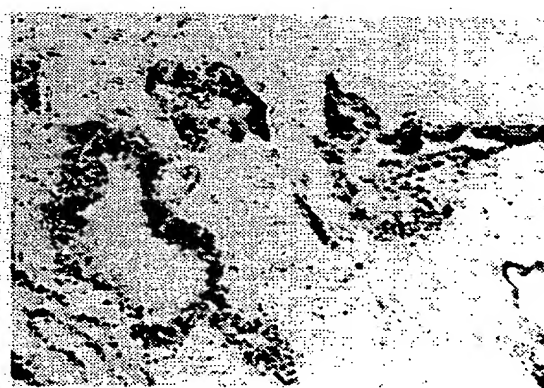
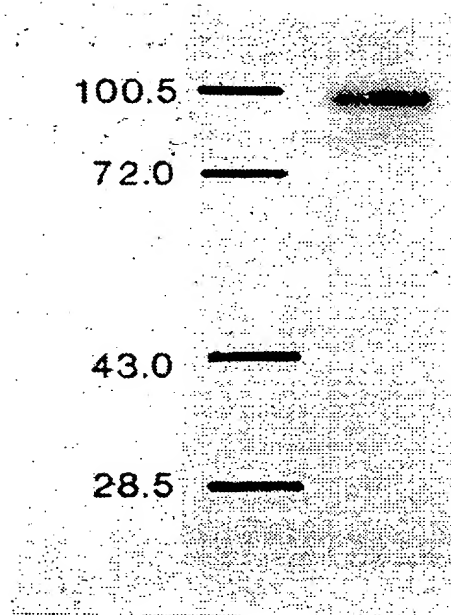


FIGURE 3D



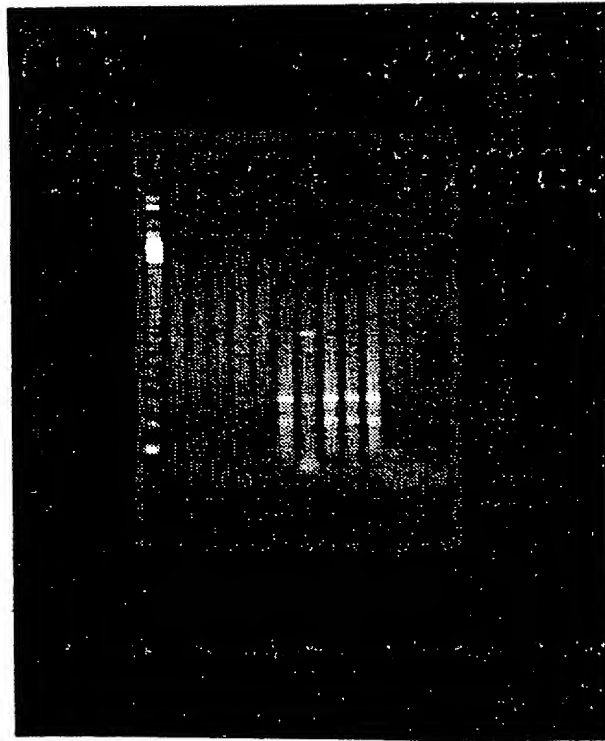
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FIGURE 4



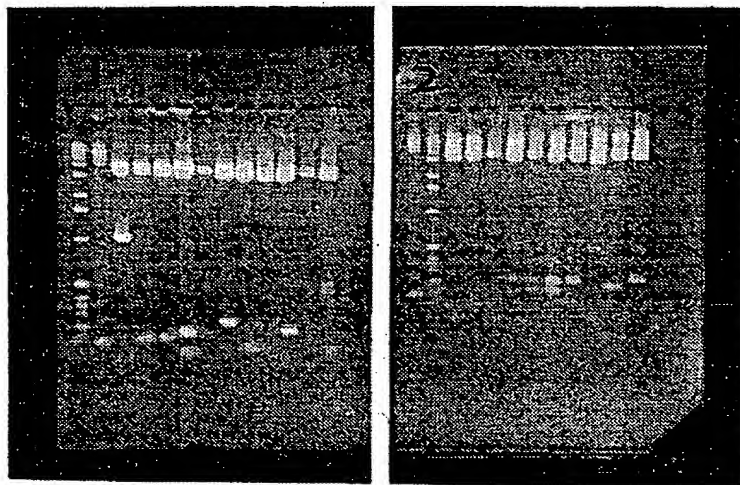
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FIGURE 5



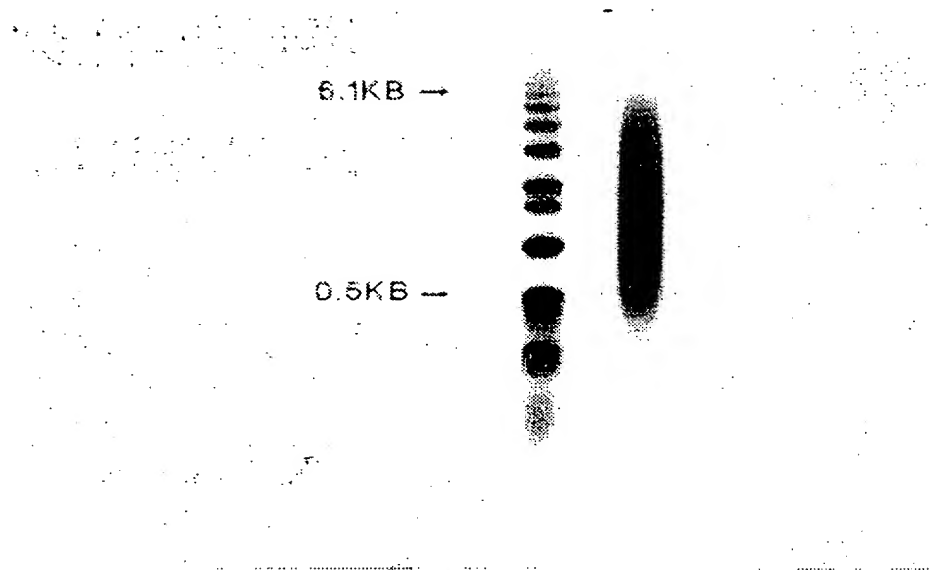
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FIGURE 6A FIGURE 6B



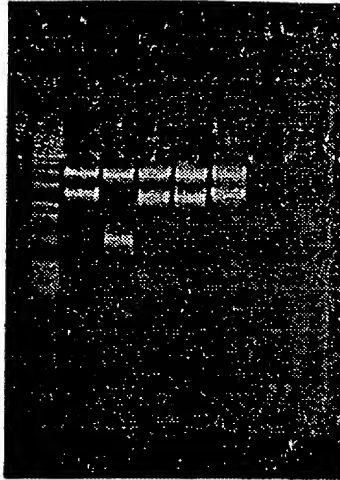
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FIGURE 7



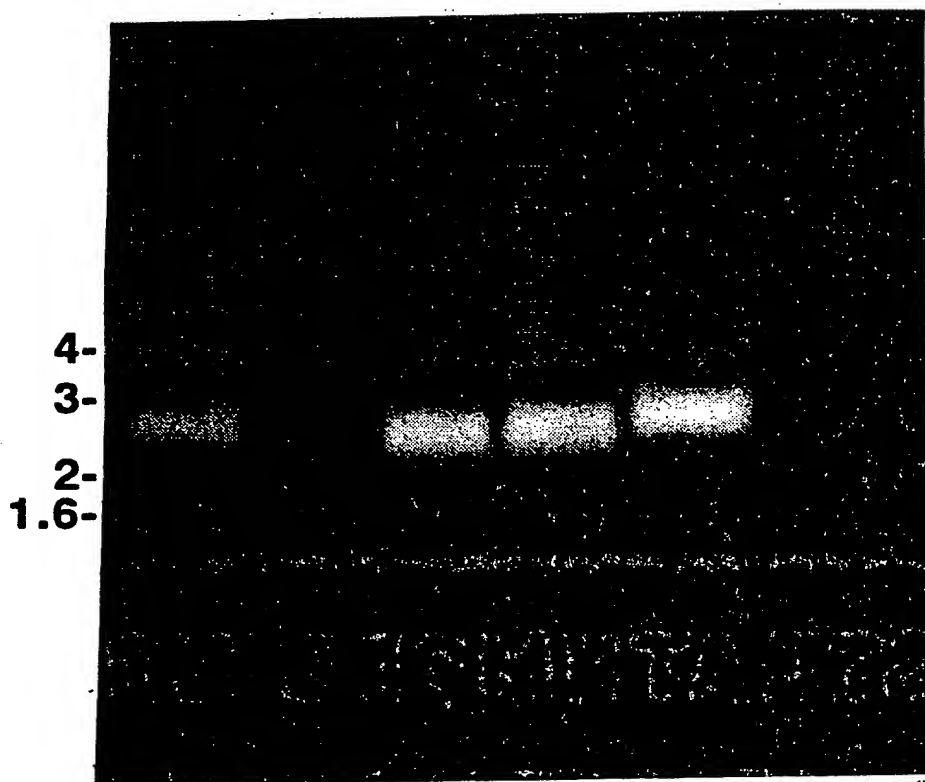
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FIGURE 8



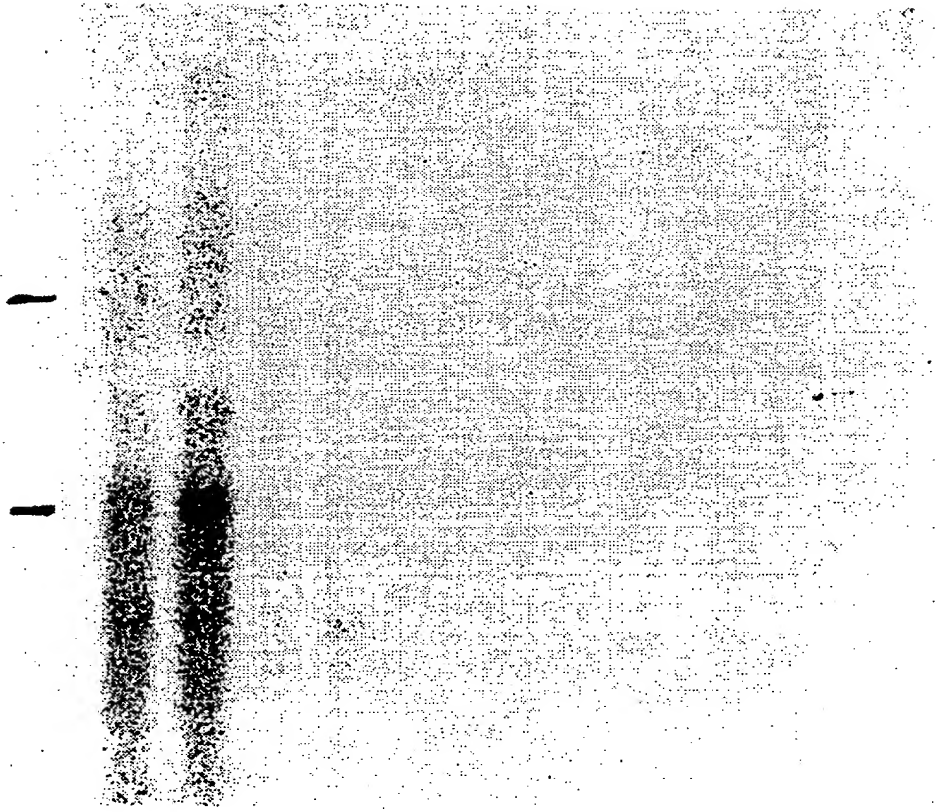
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FIGURE 9



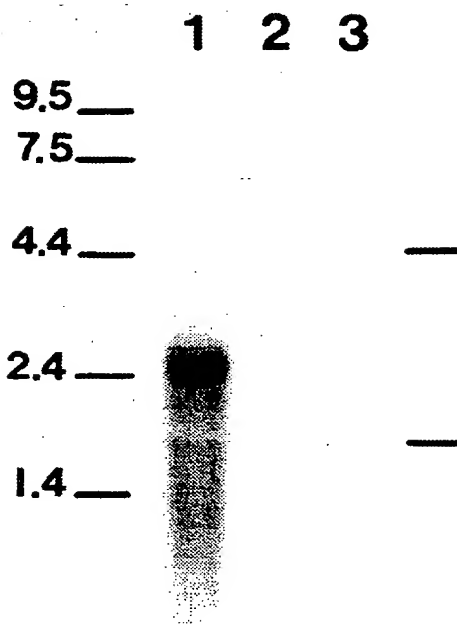
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FIGURE 10



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FIGURE 11



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FIGURE 12A

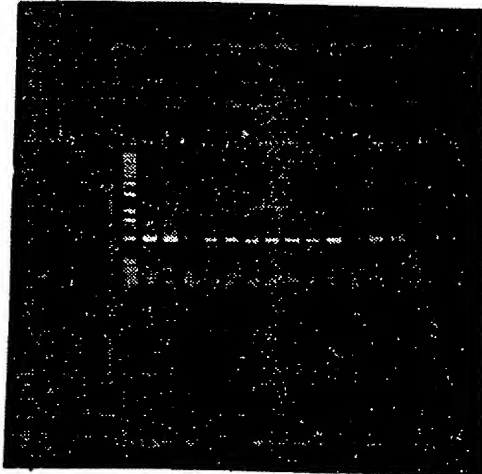
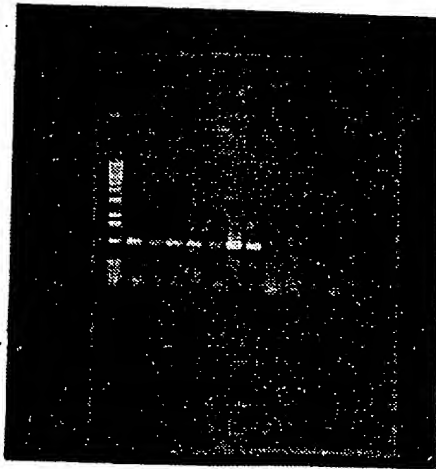
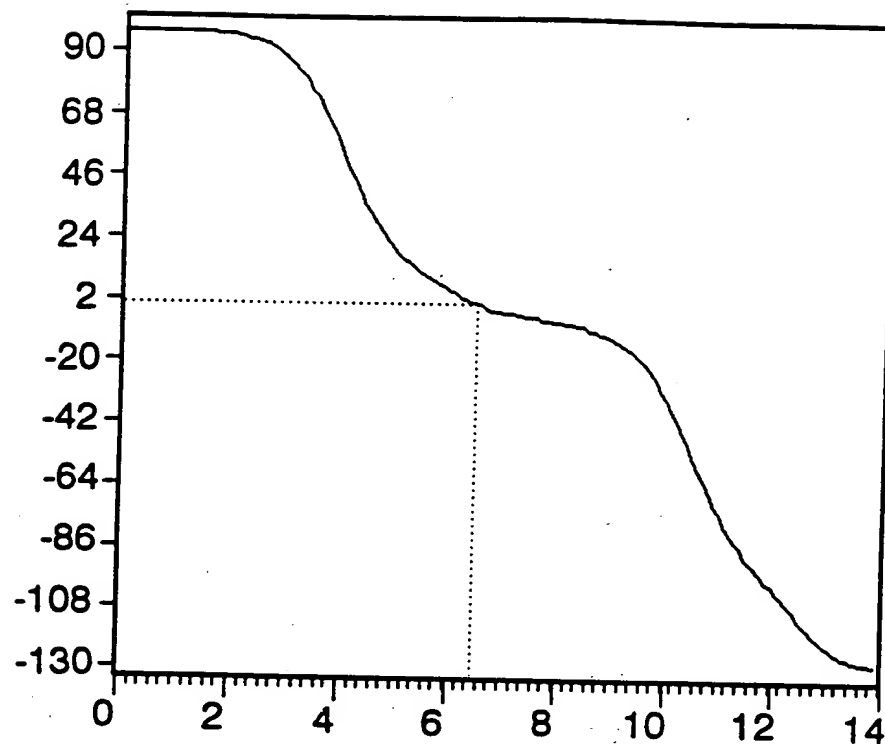


FIGURE 12B



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FIGURE 13



Analysis done on the complete sequence.

In Helical	(H)	conformation	[DC =	-75	CNAT]	:	264	AA =>	35.2%
In Extended	(E)	conformation	[DC =	-88	CNAT]	:	309	AA =>	41.2%
In Turn	(T)	conformation	[DC =	0	CNAT]	:	76	AA =>	10.1%
In Coil	(C)	conformation	[DC =	0	CNAT]	:	101	AA =>	13.4%

Sequence shown with conformation codes.

Consecutive stretch of 5 or more residues in a given conformation are overlined.

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FIGURE 14-2

91	H	H	H	H	E	H	C	E	E	T	T	C	H	H	H	H	H	H	H	E	E	E	E	E	T
121	T	T	C	C	E	E	E	E	E	E	C	T	C	C	H	E	E	E	E	T	C	C	C	T	T
151	T	E	E	E	E	E	E	E	E	E	E	T	E	C	C	T	C	C	E	E	E	E	E	E	H
181	H	H	H	H	H	H	H	H	H	H	H	H	H	T	T	T	E	E	E	E	E	E	E	E	E
211	T	T	C	C	H	H	H	H	H	H	E	E	E	E	E	E	E	T	E	E	E	E	E	E	E
241	E	E	T	T	T	E	C	T	C	T	C	E	E	E	E	E	E	E	T	T	C	E	E	E	E
271	C	C	C	E	E	E	E	H	E	E	E	E	E	E	E	E	C	E	E	E	E	E	E	E	E
301	H	H	H	H	H	H	E	T	T	C	C	C	T	E	T	T	E	T	E	E	E	E	E	E	E
331	E	E	E	C	E	C	H	H	H	H	E	E	C	C	C	C	E	E	E	E	E	E	E	E	E
361	E	E	E	E	E	E	E	E	E	E	E	E	E	C	C	C	T	E	E	E	T	C	C	C	C
391	C	H	H	H	E	E	E	H	H	H	H	C	C	C	T	T	C	C	C	T	E	E	E	E	C
421	H	H	H	H	H	H	H	C	C	C	H	H	H	H	H	H	H	H	H	H	E	E	E	E	E
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

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FIGURE 14-4

Semi-graphical output.
=====

Symbols used in the semi-graphical representation:

Helical conformation: X	Extended conformation: -
Turn conformation: >	Coil conformation: *

10	20	30	40	50
MWNLLHETDS	AVATARRPRWLCAGALVLAGGFFLLGLFGWFIKSSNEAT			
XXXXXXXXXXXXX	----->	XXXXXXXXXXXXX	----->	XXXXXXXXXXXXX
XXXXXXXXXXXXX	----->	XXXXXXXXXXXXX	----->	XXXXXXXXXXXXX
60	70	80	90	100
NITPKHNMKAFLDELKAENIKKFLYNFTQIPHLAGTEQNFQLAKQIQSQW				

FIGURE 14-5

```

XXXXXXXXXXXXXXXXXX-->-->-->-->-->-->-->-->-->-->-->-->-->-->--X*--
XXXXXXXXXXXXXXXXXX-->-->-->-->-->-->-->-->-->-->-->-->--X*--
110      |      120      130      140      150
KEFGDSVELAHYDVLLSYPNKTHPNYISINEDGNEIFNTSLFEP PPPG
-->-->-->-->-->-->-->-->-->-->-->-->-->-->-->-->-->-->-->-->
-->-->-->-->-->-->-->-->-->-->-->-->-->-->-->-->-->-->-->-->
160      |      170      180      190      200
YENVSDIVPPFSAFSPQGMPEGLVYVNVYARTEDFFKLERDMKINCSGKI

```

[illegible]

210 220 230 240 250
VIARYGVFRGNKVNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLP

GGVQRGNIILNNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYV

DAQKLEKMGSA P DSSWRGSLKVPYNVGP GFTGNFSTQKV KMHISTN

[illegible]

EVTRIYNVIGTLRGAVEPD RYVILGGHRDSWVFGIDPQSGAAVVHEIVR

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FIGURE 14-7

```

-----
-----
SFGTLKKEGWRPRRTILFASWDAEEFLLGSTEWAEENSRLQERGVAI
410      420      430      440      450
|         |         |         |         |
XXX***>>>***>-----***>----->***>***XXX-----XX
XXX***>>>***>-----***>----->***>***XXX-----XX
NADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYESWTKK
460      470      480      490      500
|         |         |         |         |
----->>-----XXX*-----XXX*-----XXX*-----*
----->>-----XXX*-----XXX*-----XXX*-----*
SPSPEFGMPRISKLGSGNDFEVFQRLGIASGRARYTKNWETNKFSGYP
510      520      530      540      550
|         |         |         |         |
***>----->***>-----XXX*----->>----->>***>-----
***>----->***>-----XXX*----->>----->>***>-----
560      570      580      590      600
|         |         |         |         |

```

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FIGURE 14-8

LYHSVYETVELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY

-----XXXXXXXXXXXXX-X-----XXXXX----->XXX
-----XXXXXXXXXXXXX-X-----XXXXX----->XXX

610 620 630 640 650
| | | | |
AVVLRKYADKIYSISMKHPQEMKTYSVSFDLSFSAVKNFTEIASKFSERL

XXXXXXXXXX-----X**XXXXX-----XXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXX-----X**XXXXX-----XXXXXXXXXXXXXXXXXXXX

660 670 680 690 700
| | | | |
QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHVIYAPSSHNKY

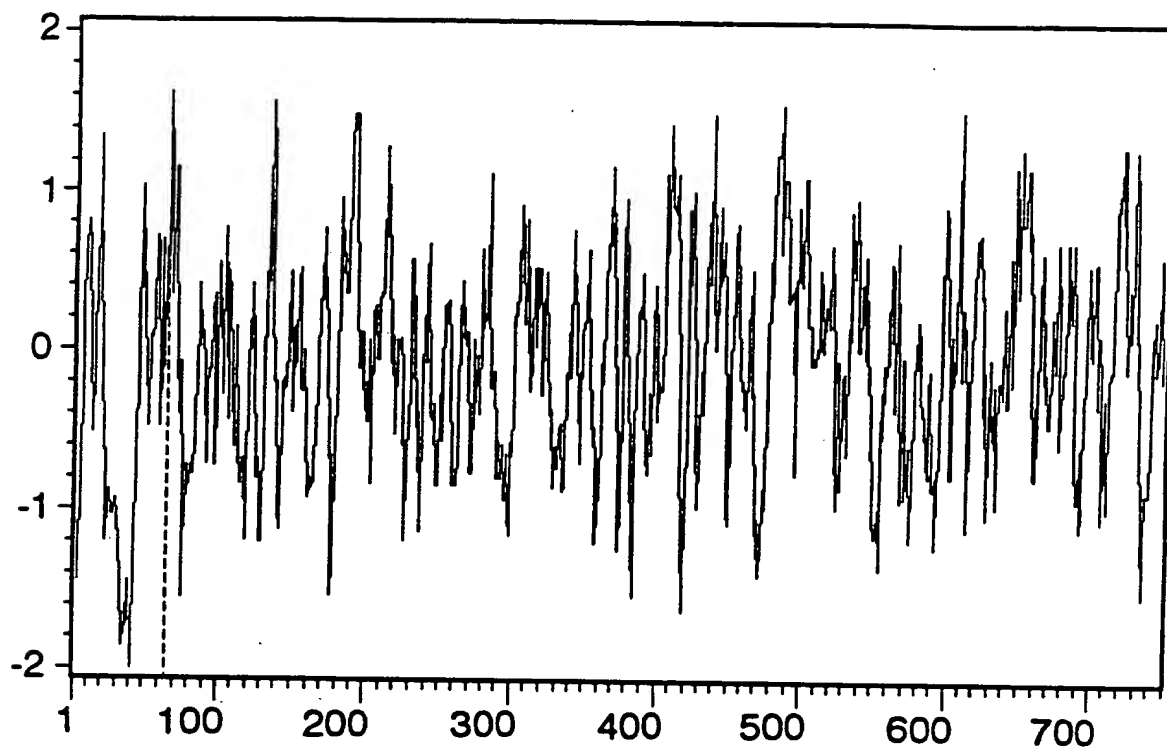
XX>>>***-----XXXXXXXXXX-->>***>----->***>
XX>>>***-----XXXXXXXXXX-->>***>----->***>

710 720 730 740 750
| | | | |
AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAETLSEVA

----->--XXXXXXXXXX***XXXXXXXXXX-----XXXXXXXXXXXXXXXXXX
----->--XXXXXXXXXX***XXXXXXXXXX-----XXXXXXXXXXXXXXXXXX

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FIGURE 15A



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FIGURE 15B

 * PREDICTION OF ANTIGENIC DETERMINANTS *

Done on sequence PMSANTIGEN.

Total number of residues is: 750.

Analysis done on the complete sequence.

The method used is that of Hopp and Woods.

The averaging group length is: 6 amino acids.

-> This is the value recommended by the authors <-

 The three highest points of hydrophilicity are:

(1)	Ah= 1.62	: From	63 to	68	: Asp-Glu-Leu-Lys-Ala-Glu
(2)	Ah= 1.57	: From	132 to	137	: Asn-Glu-Asp-Gly-Asn-Glu
(3)	Ah= 1.55	: From	482 to	487	: Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third points gave a proportion of 33% of incorrect predictions.

SUBSTITUTE SHEET (RULE 26)

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FIGURE 16-2

```

1200      1210      1220      1230      1240      1250
pmsgen AGCACCACCATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAAATGTTGGACCTGG
      : : : : : : : : : : : : : : : : : : : : : :
CHKTFE CACATGCTCTGA-AG--GTTGGAAAGGTGCGGATCCA---TTCCTGTAAGGT--GAC--AA
1170      1180      1190      1200      1210

1260      1270      1280      1290      1300      1310
pmsgen CTTTACTGGAAACTTTTCTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGT
      : : : : : : : : : : : : : : : : : : : : : :
CHKTFE CAAAGCAGGAGA----GCCAGA-TAATGGTGAAACTAGATGTGAACAATTCCCATGAAAGA
1220      1230      1240      1250      1260

1320      1330      1340      1350      1360      1370
pmsgen GACAAGAAATTACAAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAACAGACAGATATGT
      : : : : : : : : : : : : : : : : : : : : : :
CHKTFE CAGGAAGATTCTGAACATCTTCGGTGCTATCCAGGGATTGGAAGAACCTGATCGGTATGT
1270      1280      1290      1300      1310      1320

1380      1390      1400      1410      1420      1430
pmsgen CATTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCCTCAGAGTGGAGC
      : : : : : : : : : : : : : : : : : : : : : :
CHKTFE TGTGATTGGAGCCACAGAGAGACTCCTGGGGCCCCAGGAGTGGCTAAAGCTGGCAGCTGGAAC
1330      1340      1350      1360      1370      1380

```

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	1680	1690	1700	1710	1720	1730
pmsgen	TACAGCTTGGTACACAACCTAACAAAGAGCTGAAAAGCCCTGATGAAGCCTTTGAAGGC					
	:: :: :	:	: : :	: : : :	: : : :	: : :
CHKTFE	TATATGCTGGGGAGTATTATGAAGGGGTGAAGAATCCAGCACGACTCTCAGAGAGC					
	1630	1640	1650	1660	1670	1680

```

1740      1750      1760      1770      1780      1790
pmsgen  AAATCTCTTTATGAAGTTGGACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCC
      : : : : : : : : : : : :
CHKTFE  ----CTCTATAACAGACTTGGCCAGACTGGGTAAAGCAGTTGTTCCCTCTTGGCCCTGGA
      1690      1700      1710      1720      1730

```

FIGURE 16-5

RATRRR Rat transferrin receptor mRNA, 3' end. 164 164 311
55.5% identity in 560 nt overlap

1210 1220 1230 1240 1250
pmsgen CCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAAGTGCCCTACAAATGTTGGACCCTGGCTT-

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RATRRF TGCAGAAAGCTATTCAAAACATGGGAAGGAACTGTCCCTCCTAGTTGGAAATATAGATTC
610 620 630 640 650 660

1260 1270 1280 1290 1300 1310
pmsgen -TACTGGAAACTTTTCTACACAAAGTCAAGATGCACATC-CACTCT-ACCAATG----

RATRRF CTCATGTAAGCTGGAACCTTTCACAGAAATCAAAATGTGAAGCTCACTGTGAACAAATGTACT
670 680 690 700 710 720

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FIGURE 16-9

Accession	Human transferrin receptor mRNA, complete cd	145	145	266
HUMTFRR	54.3% identity in 464 nt overlap			

```

1280      1290      1300      1310      1320      1330
pmsgen AAAAGTCAAGATGCACATC-CACTCT-ACCAATG-----AAGTGACAAGAAATTACAA
: : : : : : : : : : : : : : : : : : : : : : : : : :
HUNTER AGAAAGCAAGAAATGTGAAGCTCACTGTGAGCAATGTGCTGAAAGAGATAAAAATTCTTAA
1200      1210      1220      1230      1240      1250

```

	1400	1410	1420	1430	1440	1450
pmsgen	CCGGACTCATGGGTGTTGGTGTATTGACCTCAGAGT-GGAGCAGCTGTTGTTTCATG					
	: :	: : : : : :	: :	: : : : : :	: : : : : :	: :
HUMTFR	GAGAGATGCATGGGGCCCTGGAGCTGCAAAATC-CGGTGTAGGCACAGCTCTCCTATTGA					
	1320	1330	1340	1350	1360	1370

pmsgen ATAGAAGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACA-GCTTGGT-AC
:
HUNTFR GTTCTTGGTACCAGCAACTTCAAGGTTTCTGCCAGCCCACTGTTGTATACGCTTATTGAG

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FIGURE 16-11

1690	1700	1710	1720	1730	1740
pmsgen	ACAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGAAGGCAAA	TCTCTTATG			
:	:	:	:	:	:
HUMTFR	AAAACAATGC	AAATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC			
1620	1630	1640	1650	1660	1670

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FIGURE 17A

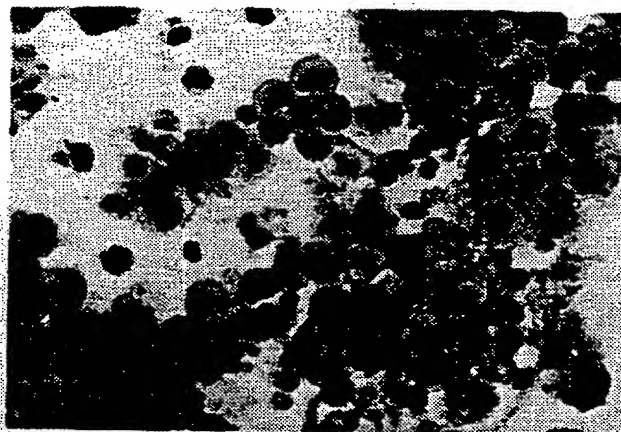


FIGURE 17B

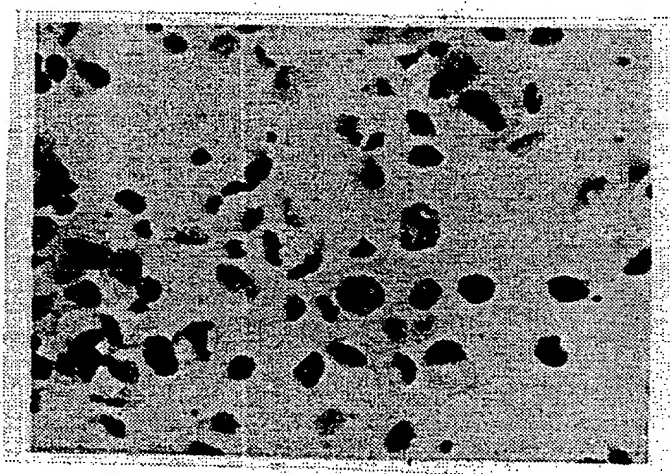
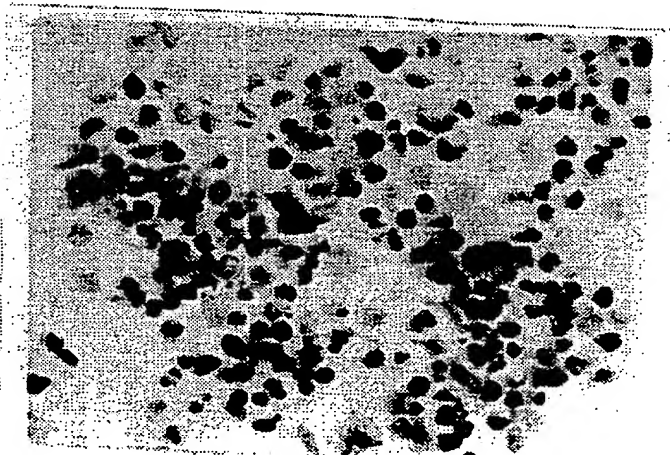
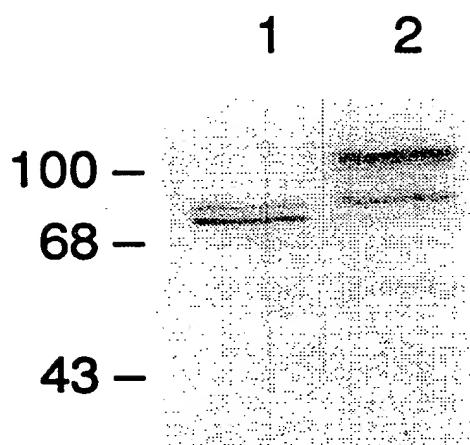


FIGURE 17C



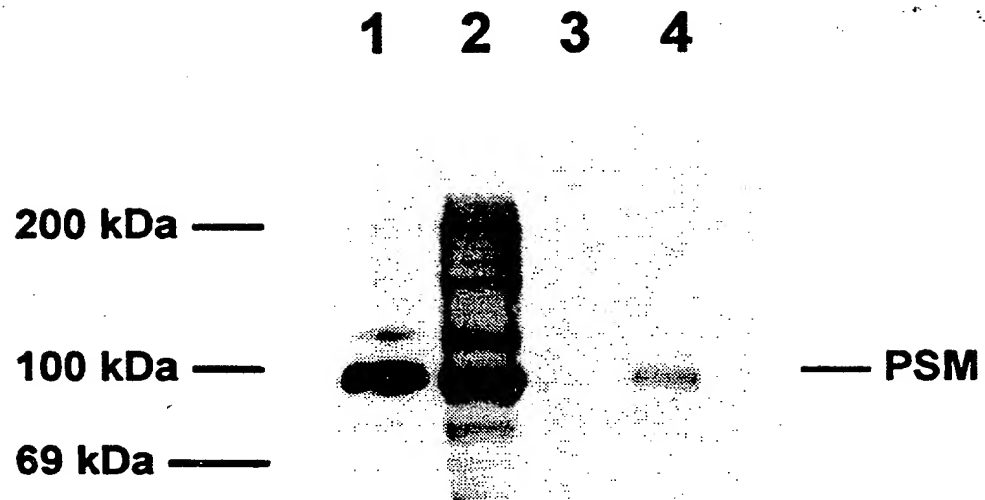
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FIGURE 18



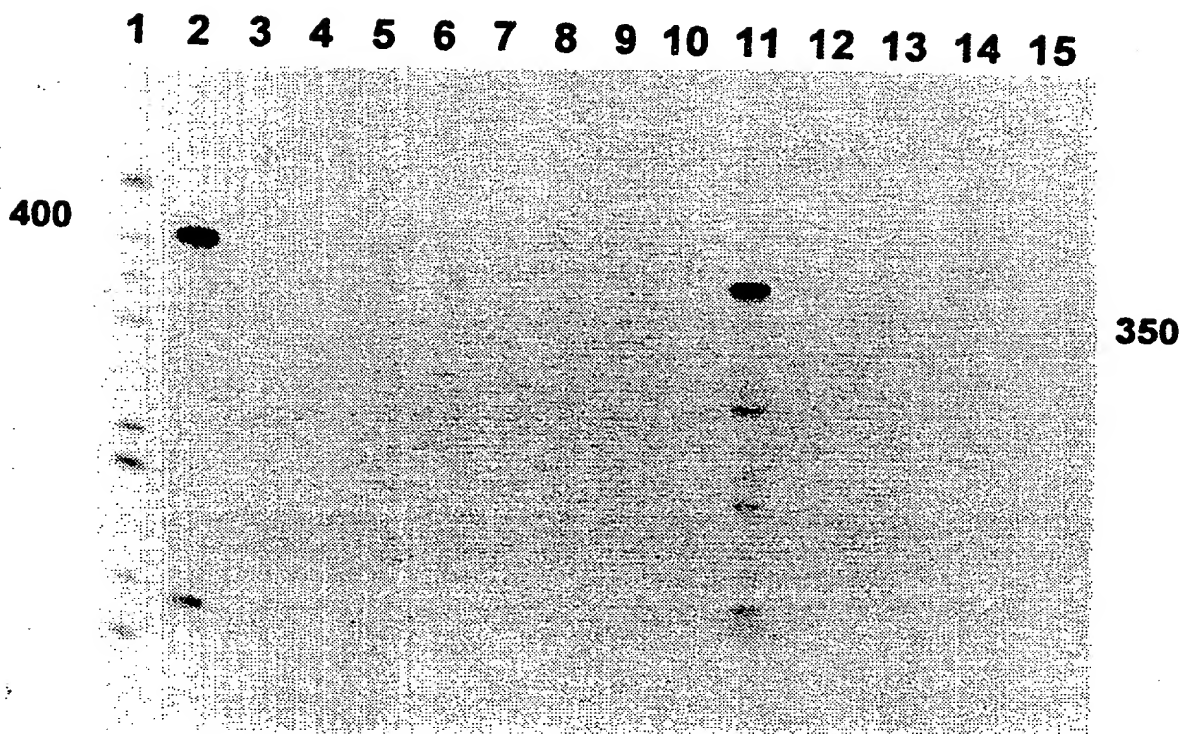
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FIGURE 19



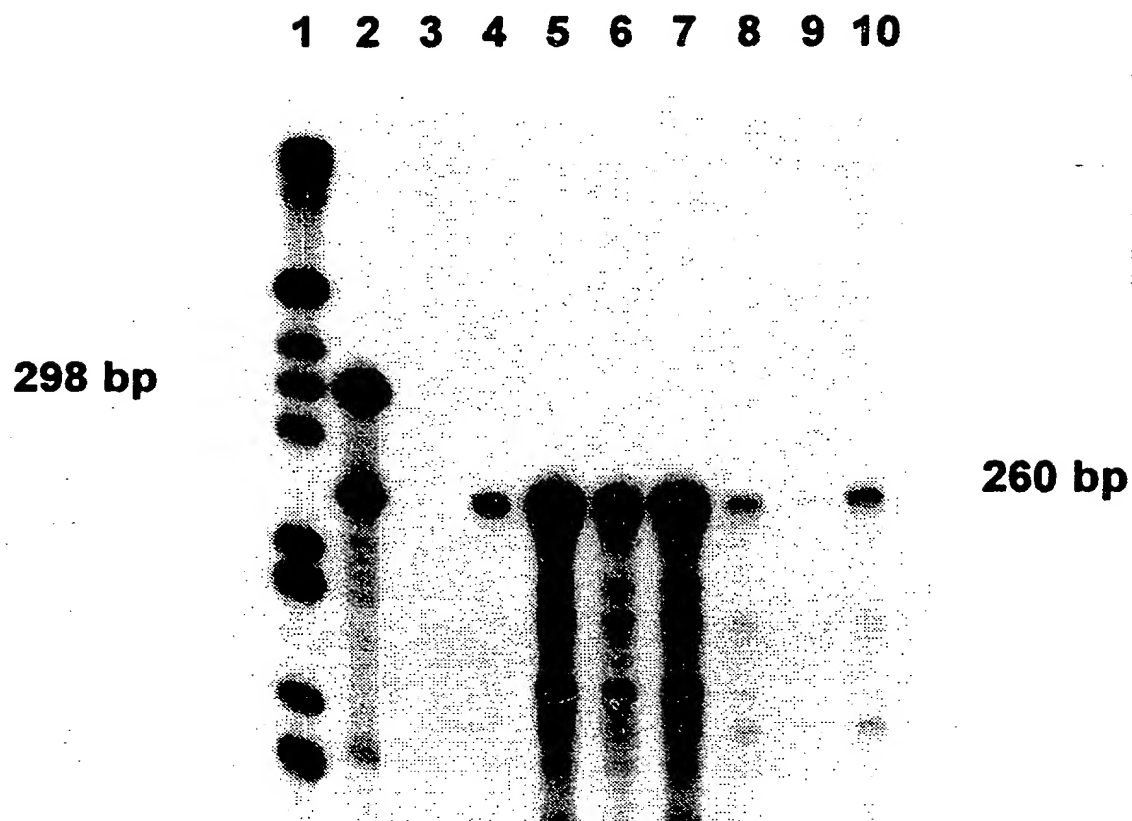
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FIGURE 20



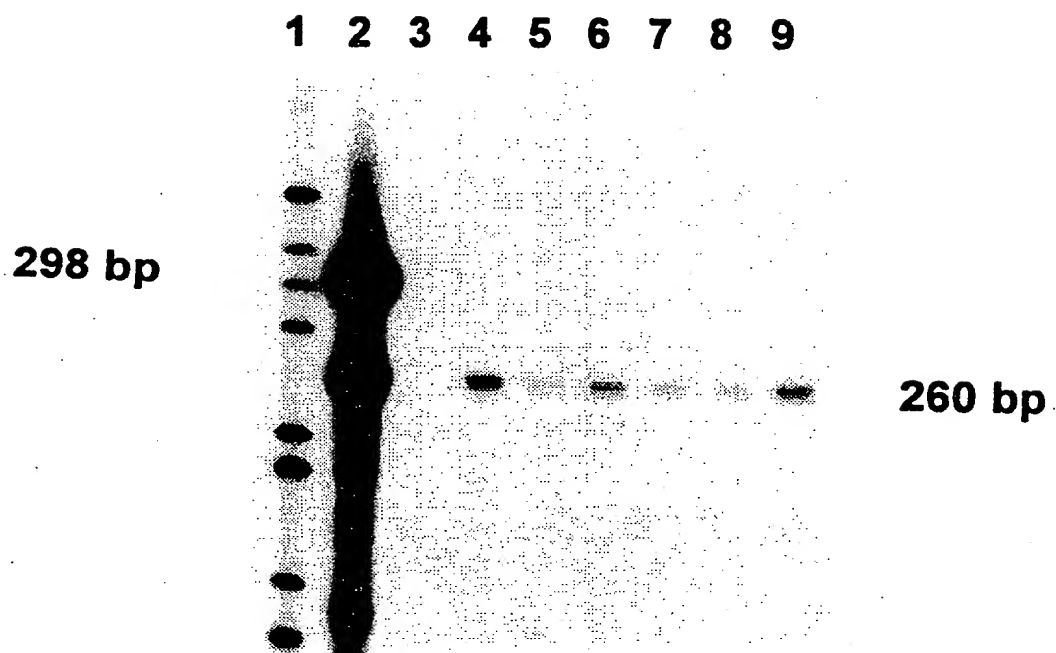
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FIGURE 21



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FIGURE 22



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FIGURE 23

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

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FIGURE 24A

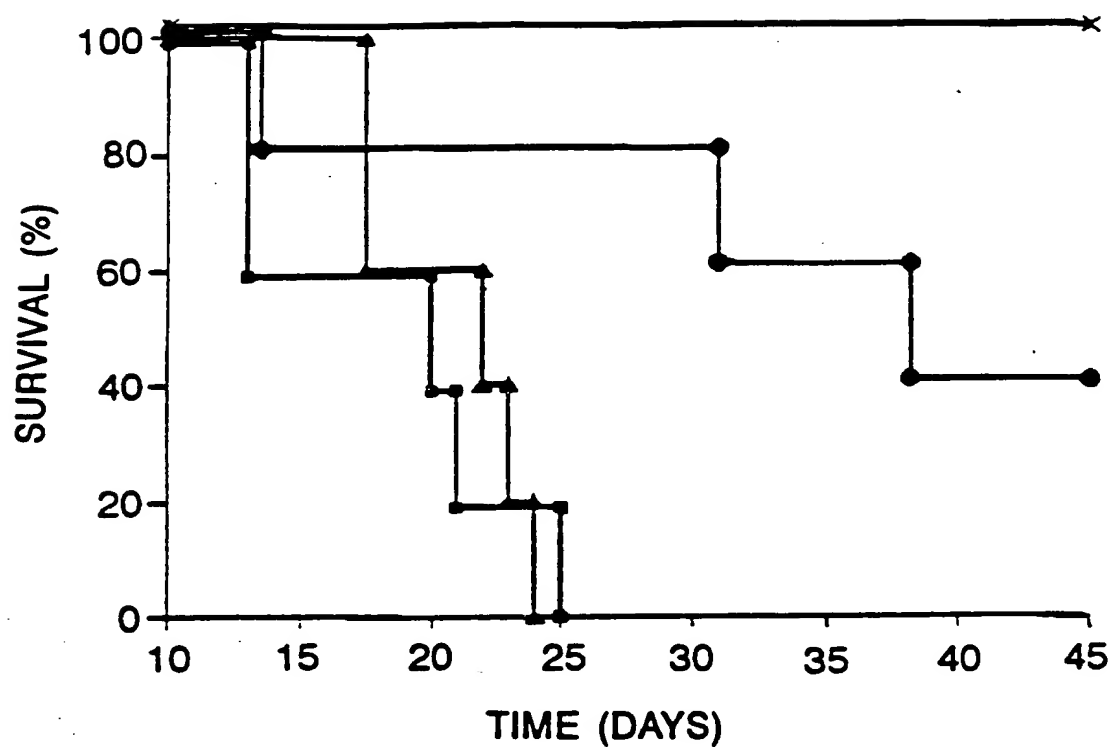
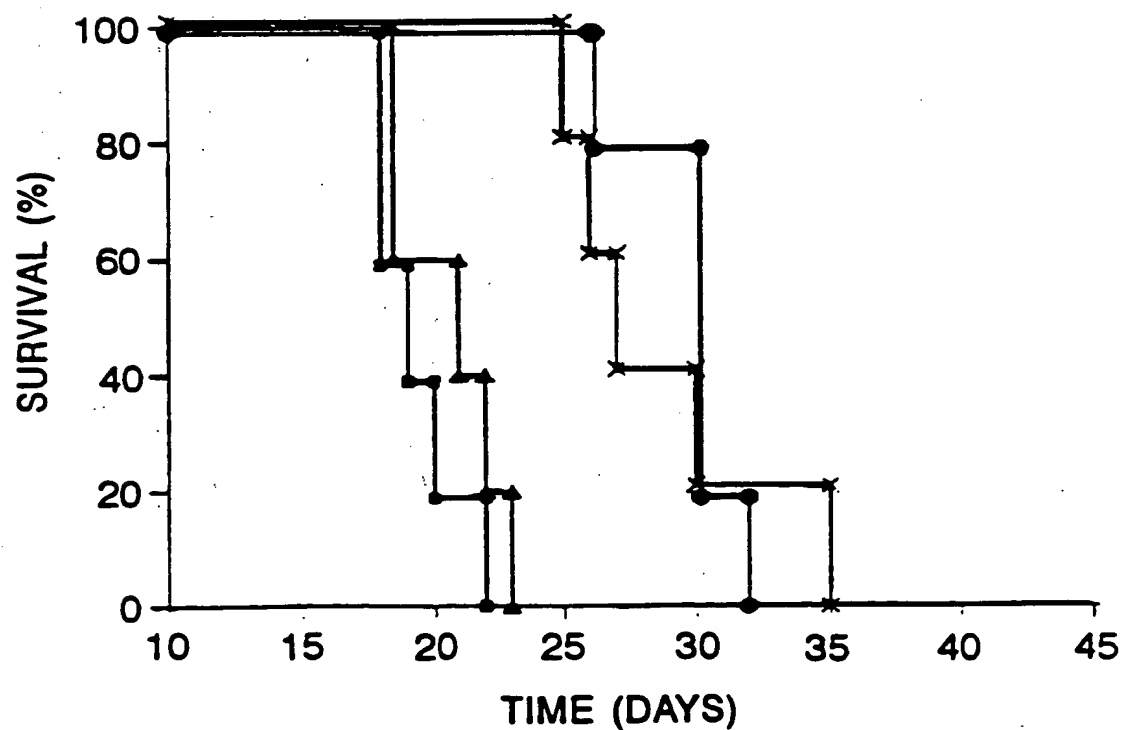


FIGURE 24B



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FIGURE 25A

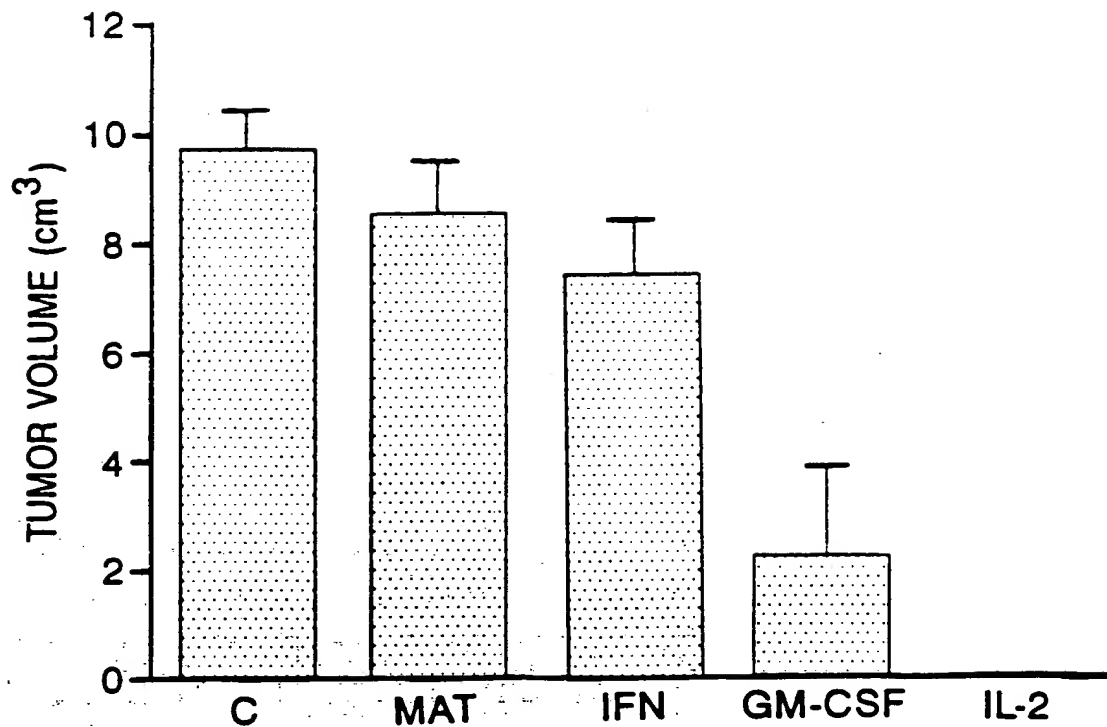
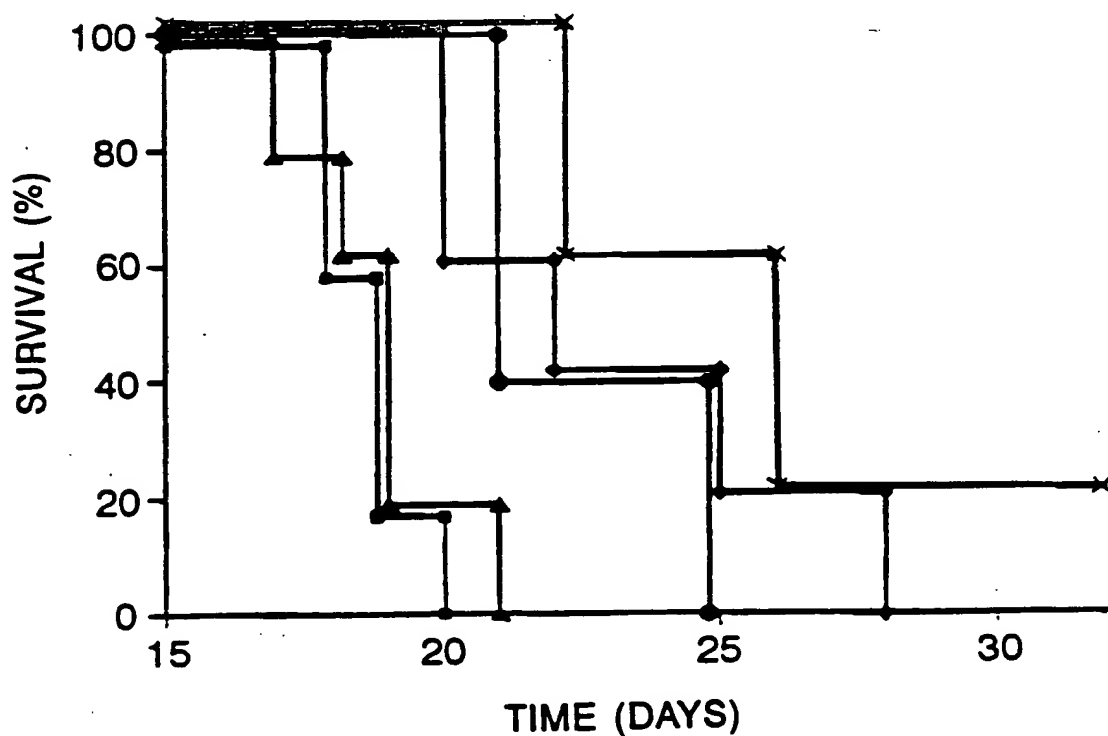
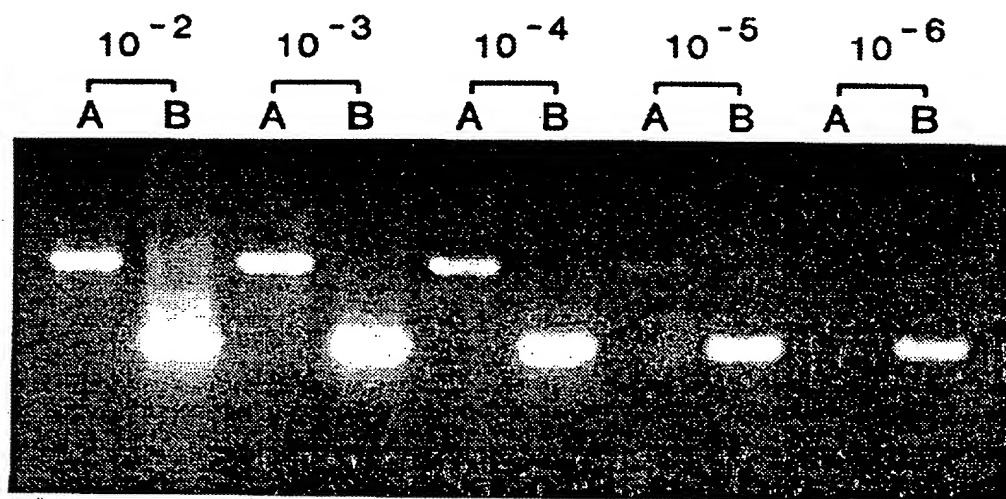


FIGURE 25B



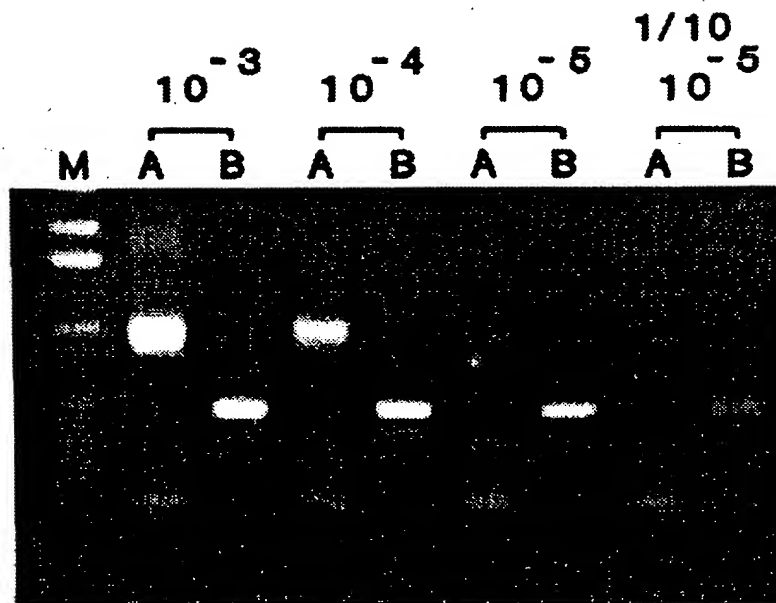
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FIGURE 26



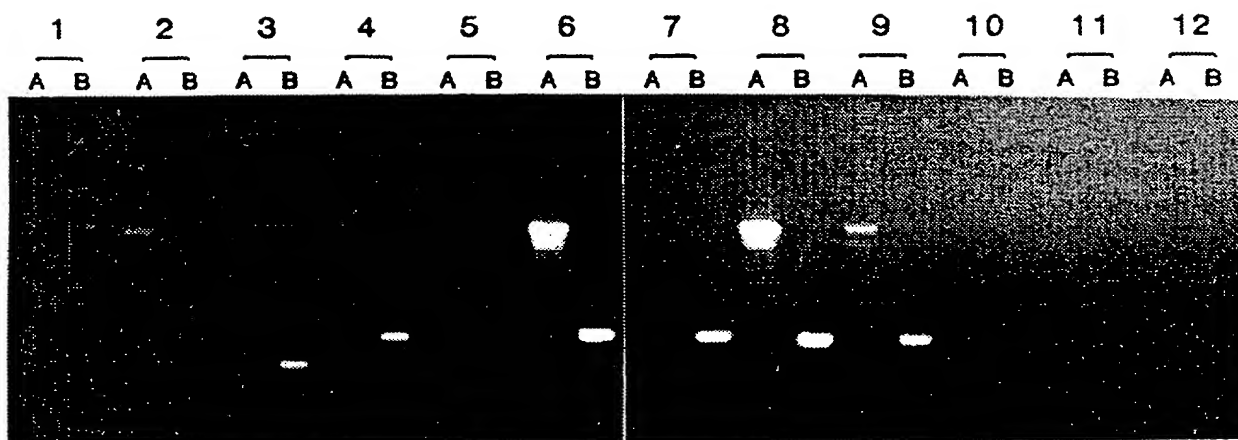
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FIGURE 27



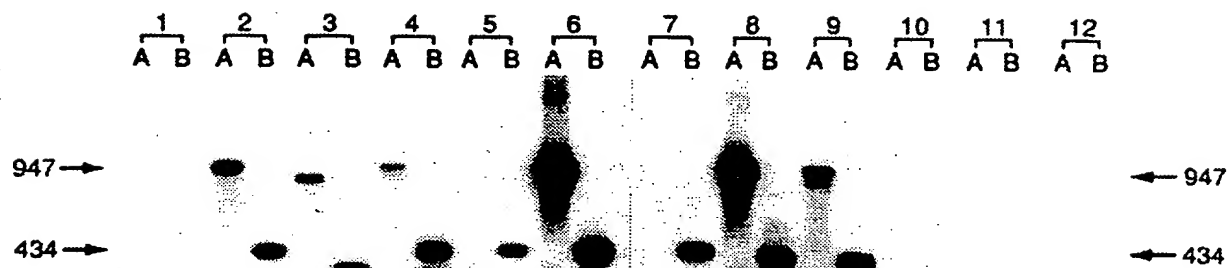
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FIGURE 28



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FIGURE 29



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FIGURE 30

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	-	+
2	T2NoMo	RRP 7/93	6.1	-	-	+
3	T2CNoMo	PLND 5/93	4.5	0.1	-	+
4	T2BNoMo	RRP 3/92	NMA	0.4	-	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	-	+
6	Recur T3	I-125 1986	54.7	1.4	-	+
7	T3ANoMo	RRP 10/92	NMA	0.3	-	+
8	T3NxMo	XRT 1987	7.5	0.1	-	-
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-
10	D2	S/P XRT Flutamide + Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	-	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-
15	D1	Proscar + Flutamide	20.8	0.5	-	-
16	T2CNoMo	RRP 4/92	0.1	0.3	-	-